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Nucleotide sequence coding for an outer membrane protein from *Neisseria meningitidis* and use of said protein in vaccine preparations

### Abstract:

The present invention is concerned with a method for the isolation of a nucleotide sequence which codes for a protein having a molecular weight of about 64 000 daltons, which is located on the outer membrane of *N. meningitidis*, as well as with the recombinant DNA obtained therefrom, which is used for the transformation of a host microorganism. The technical object pursued with the invention is the identification of a nucleotide sequence coding for a highly conserved and common protein for the majority of pathogenic *Neisseria* strains, the production of this protein with a high level of purity and in commercially useful amounts using the recombinant way, so that it can be used in diagnostic methods and vaccine preparations with a broad immunoprotection spectrum.

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(54) Nucleotide sequence coding for an outer membrane protein from *Neisseria meningitidis* and use**EP 0 474 313 A2**

of said protein in vaccine preparations.

⑤7 The present invention is concerned with a method for the isolation of a nucleotide sequence which codes for a protein having a molecular weight of about 64 000 daltons, which is located on the outer membrane of *N. meningitidis*, as well as with the recombinant DNA obtained therefrom, which is used for the transformation of a host microorganism. The technical object pursued with the invention is the identification of a nucleotide sequence coding for a highly conserved and common protein for the majority of pathogenic *Neisseria* strains, the production of this protein with a high level of purity and in commercially useful amounts using the recombinant way, so that it can be used in diagnostic methods and vaccine preparations with a broad immunoprotection spectrum.

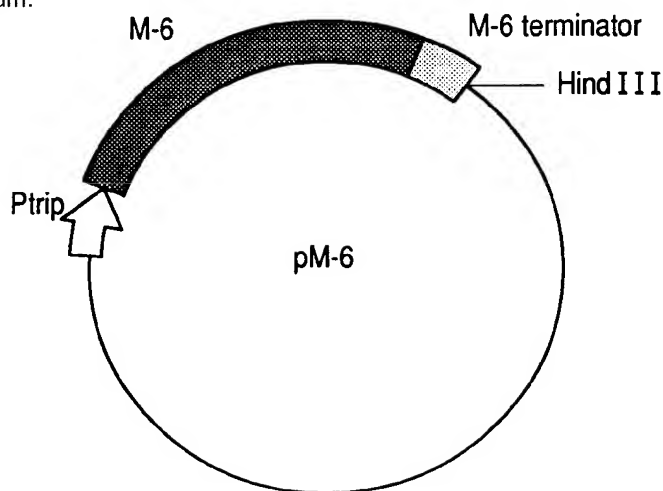


FIG. 1

The present invention is in the field of Genetic Engineering and Biotechnology. More in particular, the invention is related to a nucleotide sequence obtained from the pathogenic bacterium *Neisseria meningitidis*, which nucleotide sequence codes for a protein belonging to the outer membrane of said bacterium. Said protein is cloned and expressed in the host *Escherichia coli*. The characteristics of this protein as well as its capacity to induce immunologically active antibodies (bactericidal antibodies) in its natural host, allow its use in vaccine preparations against pathogenic strains of this microorganism.

The gram-negative bacterium *N. meningitidis* is responsible for one of every three cases of bacterial meningitis in the world. It was described for the first time by Anton Weichselbaum in 1887 (I. DeVoe, 1982, *Microbiol. Revs.* 46: 162-190), and man (i.e. human beings) is its only natural host up to date.

In the first half of this century some essential aspects were found in relation to the metabolism and serological differentiation of this microorganism. The first unsuccessful attempts to obtain vaccine preparations were based on its capsular polysaccharide (E. Kabat et al., 1945, *J. Exp. Med.* 80: 299-307). According to the chemical composition of this capsular polysaccharide, the bacterium *N. meningitidis* is serogrouped in A, B, C, 29-E, H, I, K, L, W-135, X, Y or Z, and the major percentage of illness is caused by A, C, Y, W-135 and B. Non-encapsulated strains are not associated with the invasive disease.

Using different methods of purification of these polysaccharides (E. Gotschlich et al., 1969, *J. Exp. Med.* 129: 1349-1365) the four first polysaccharides (PS) showed to be good immunogens and inducers of bactericidal antibodies in humans (E. Gotschlich et al., 1969, *J. Exp. Med.* 129: 1367-1384). The presence of this kind of antibodies has been correlated previously with non-susceptibility to the infection (I. Goldschneider et al., 1969, *J. Exp. Med.* 129: 1307-1326). As of today mono-, bi- or tetravalent vaccines have been well studied for serotypes A, C and W-135 (F. Ambrosch et al., 1983, *Bulletin of the WHO* 61: 317-323; I. Vodopija et al., 1983, *Infect. Immunol.* 42: 599-604; M. Cadoz et al., 1985, *Vaccine* 3: 340-342; H. Peltola et al., 1985, *Pediatrics* 76: 91-96).

These vaccines have been licensed for their use in humans in different countries (Centers for Disease Control, 1985, *Morbidity and Mortality Weekly Report* 34: 255-259) and some of them are commercially available from different firms and producers (Connaught Laboratories, USA; Smith Kline-RIT, Belgium; Institute Merieux, France; Behringwerke Aktiengesellschaft, Germany; Istituto Sieroterapico e Vaccinazione Toscana "Sclavo", Italy; Swiss Serum and Vaccine Institute, Berne, Switzerland; among others).

However, the conventional vaccine against *N. meningitidis* serogroup C does not induce sufficient levels of bactericidal antibodies in children under 2 years old, which are the principal victims of this disease. It has been demonstrated that the titer of specific antibodies against *N. meningitidis* in children under four years of age, after three years of vaccination, is similar in vaccinated and in non-vaccinated ones (H. Kayhty et al., 1980, *J. of Infect. Dis.* 142: 861-868). Also, no memory response was found against *N. meningitidis* after 8 years of vaccination in young adults (N. Rautonen et al., 1986, *J. of Immunol.* 137: 2670-2675).

The polysaccharide corresponding to *N. meningitidis* serogroup B is poorly immunogenic (E. Gotschlich et al., 1969, *J. Exp. Med.* 129: 1349-1365) and induces a poor response of IgM of low specificity (W. Zollinger et al., 1979, *J. Clin. Invest.* 63: 836-848). There are different theories related to this problem, such as cross-reactivity between B polysaccharide and fetal brain structures, antigenic structures modified in solution and sensitivity to neuroaminidases (C. Moreno et al., 1985, *Infect. Immun.* 47: 527-533). Recently, a chemical modification of PS B was achieved, which induced a response in the host (H. Jennings et al., 1988, *US Patent* 4 727 136; F. Ashton et al., 1989, *Microb. Pathogen.* 6: 455-458), but safety of this vaccine in humans has not been demonstrated.

Due to the lack of an effective vaccine against *N. meningitidis* B, and because the risk of endemic infection is low and mainly restricted to children, a routine immunization with polysaccharides is not recommended (C. Frasch, 1989, *Clin. Microbiol. Revs.* 2: S134-S138) except in the case of an epidemic.

Since after the Second World War the disease was caused in most of the cases by *N. meningitidis* B, vaccines against serogroup B gained special significance.

Other outer membrane components of *N. meningitidis* include phospholipids, lipopolysaccharides (LPS or endotoxins), pili proteins and others. Different immunotypes of LPS have been described for *N. meningitidis* (W. Zollinger and R. Mandrell, 1977, *Infect. Immun.* 18: 424-433; C.M. Tsai et al., 1983, *J. Bacteriol.* 155: 498-504) and immunogenicity using non-toxic derivatives was assayed (H. Jennings et al., 1984, *Infect. Immun.* 43: 407-412) but their variability (H. Schneider et al., 1984, *Infect. Immun.* 45: 544-549) and pyrogenicity (when it is conjugated to lipid A) are limiting factors up to now.

The pili, structures needed to fix cells to nasopharyngeal mucous membrane (D. Stephens et al., 1983, *The J. Infect. Dis.* 148: 369-376) have antigenic diversity among different strains (J. Greenblatt et al., 1988, *Infect. Immun.* 56: 2356-2362) with some common epitopes (D. Stephens et al., 1988, *The J. Infect. Dis.* 158: 332-342). Presently there are some doubts in relation to the effectiveness of a vaccine based on these structures. However some of these types of vaccine have been obtained, without known results related to

their use in humans (C. Brinton, 1988, US Patent 4 769 240).

Recently, the attention has switched to the other proteins of the outer membrane of this bacterium. There are many immunological types of these protein complexes.

The strains of *N. meningitidis* are subdivided in serotypes according to the presence of specific epitopes in the majoritary protein P1/P2 and in subtypes according to other epitopes in protein P1 (C. Frasch et al., 1985, Rev. Infect. Dis. 7: 504-510).

There are several published articles and patent applications concerning vaccines based on cocktails of these proteins, with previous selective removal of endotoxins using biocompatible detergents. The immunogenicity of these cocktails in animals and humans has been demonstrated (W. Zollinger et al., 1979, J. Clin. Invest. 63: 836-848; C. Frasch and M. Peppler, 1982, Infect. Immun. 37: 271-280; E. Beuvery et al., 1983, Infect. Immun. 40: 369-380; E. Rosenqvist et al., 1983, NIPH Annals 6: 139-149; L. Wang and C. Frasch, 1984, Infect. Immun. 46: 408-414; C. Moreno et al., 1985, Infect. Immun. 47: 527-533; E. Wedege and L.

Froholm, 1986, Infect. Immun. 51: 571-578; C. Frasch et al., 1988, The J. Infect. Dis. 158: 710-718; M. Lively and Z. Wang, 1988, Infect. Immun. 56: 3221-3227; J. Poolman et al., 1988, In J. Poolman et al (Eds), Gonococci and Meningococci, Kluwer Academic Publishers, Dordrecht, The Netherlands, pp 159-165; E. Rosenqvist et al., 1988, J. Clin. Microbiol. 26: 1543-1548), including results in massive field trials e.g. Capetown, South Africa in 1981 (C. Frasch, 1985, Eur. J. Clin. Microbiol. 4: 533-536); Iquique, Chile, 1987 (W. Zollinger, 1988, Proceedings of the Sixth International Pathogenic Neisseria Conference. Callaway Gardens Conference Center) and Cuba 1986 and 1988 (G. Sierra, 1988, Proceedings of the Sixth International Pathogenic Neisseria Conference. Callaway Gardens Conference Center). However, with the exception of the last case, the bactericidal antibodies induced by these preparations were restricted to the same serotype strains or related ones.

One of these vaccines is referred to in US patent 4,601,903 which is restricted to one of the *Neisseria* types producing meningitis (serotype 2), with a high incidence, but also other serotypes have been isolated with high frequency from patients, such as serotypes 4 (Cuba from 1981 to 1983, H. Abdillahi et al., 1988, Eur. J. Clin. Microbiol. Infect. Dis. 7: 293-296; Finland from 1976 to 1987, H. Kayhty et al., 1989, Scand. J. Infect. Dis. 21: 527-535); 8 (Australia from 1971 to 1980, F. Ashton et al., 1984, Can. J. Med. Biol. 30: 1289-1291) and 15 (Norway from 1982 to 1984, L. Froholm et al., 1985, Proceedings of the Fourth International Symposium on Pathogenic Neisseria. American Society for Microbiology; Chile from 1985 to 1987, S. Ruiz et al., 1988, Proceedings of the Sixth International Pathogenic Neisseria Conference. Callaway Gardens Conference Center) as well as strains of undefined serotype (F. Ashton et al., 1980, Can. J. Microbiol. 26: 1480-1488; Australia from 1971 to 1980, F. Ashton et al., 1984, Can. J. Med. Biol. 30: 1289-1291; Finland from 1976 to 1987, H. Kayhty et al., 1989, Scan. J. Infect. Dis. 21: 527-535).

The Cuban vaccine achieved in 1988 by the Centro Nacional de Biopreparados (European Patent Application. No. 301 992) has proven to be very effective. It is based on a high molecular weight antigenic complex. It possesses a broad range of cross-reactivity with other strains and produces and maintains bactericidal antibodies in the immunized host.

However, the methods employed to obtain this type of vaccine start with the multiplication in an appropriate culture of a microorganism which is highly pathogenic, with the associated biological risk of handling directly the bacteria. Moreover, this kind of preparation contains lipopolysaccharides, a contaminant that, although it may increase the product's effectiveness, shows at the same time undesirable secondary effects because of its powerful pyrogenicity. Also, its variation in minor antigenic components, which form part of the preparation, cannot be controlled in the different batches, which makes it difficult to follow important parameters related to the reactogenicity and immunogenicity.

For this reason, there is increasing interest in the identification of nucleotide sequences coding for highly conserved proteins in all strains, and even more so the identification of inducer proteins of bactericidal antibodies common to the majority of pathogenic *Neisseria*, in order to obtain vaccine preparations with a broad spectrum of protection.

There are different proteins with high molecular weight which are present in low amounts in the outer membrane of *N. meningitidis* when this microorganism is grown in conventional culture media but have a strong response in affected individuals (J. Black et al., 1986, Infect. Immun. 54: 710-713; L. Aoun et al., 1988, Ann. Inst. Pasteur/ Microbiol. 139: 203-212) and/or increase their response under special culture conditions (J. van Putten et al., 1987, Antoine van Leeuwenhoek 53: 557-5564; A. Schryvers and L. Morris, 1988, Molecular Microbiol. 2: 281-288 and Infect. Immun. 56: 1144-1149). Some of these proteins are highly conserved among the different strains, in particular those related to the acquisition of iron by the microorganism, that have become interesting vaccine candidates (L. Mocca et al., 1988, Proceedings of the Sixth International Pathogenic Neisseria Conference. Callaway Gardens Conference Center; C. Frasch,

1989, Clin. Microbiol. Revs. 2: S134-S138).

In addition to pure proteins obtained from the micro-organism or strains of related species (e.g. 37 kD protein, T. Mietzner and S. Morse, 1987, US Patent 4 681 761), several related genes have been cloned and expressed. Among these proteins are the following:

- 5 protease IgAI (J. Koomey and S. Falkow, 1984, Infect. Immun. 43: 101-107);
- protein P1 (A. Barlow et al., 1987, Infect. Immun. 55: 2734-2740, and 1989, Molec. Microbiol. 3: 131-139);
- protein P5a (T. Kawula et al., 1988, Infect. Immun. 56: 380-386);
- protein P5c (T. Olyhoek and M. Achtman, 1988, Proceedings of the Sixth International Pathogenic N. Conference. Callaway Gardens Conference Center);
- 10 protein P4 (K. Klugman et al., 1989, Infect. Immun. 57: 2066-2071);
- protein P2 (K. Murakami et al., 1989, Infect. Immun. 57: 2318-2323);
- and from *N. gonorrhoeae*, which code for proteins with cross-reactivity with their corresponding proteins from *N. meningitidis*:
- antigen H.8 (W. Black and J.G. Cannon, 1985, Infect. Immun. 47: 322-325);
- 15 macromolecular complex (W. Tsai and C. Wilde, 1988, Proceedings of the Sixth International Pathogenic Neisseria Conference. Callaway Gardens Conference Center);
- 37 kDa protein, repressed in the presence of iron (S. Berish et al., 1988, Proceedings of the Sixth International Pathogenic Neisseria Conference. Callaway Gardens Conference Center).

The use of these proteins as active vaccine preparation has not been reported or the bactericidal tests of antibodies induced against them were negative, such as in the case of mouse monoclonal antibodies against H.8 (J. Woods et al., 1987, Infect. Immun. 55: 1927-1928).

Up to the moment, the protein P1 located in the outer membrane of *N. meningitidis* is one of the best characterized and studied antigens. This protein presents no variability within the same strain. However, there are more than 17 types of proteins P1 in *Neisseria* which have differences in three variable regions, 25 this being the basis of the classification of *N.* in different subtypes. This protein is very immunogenic in humans (W.D. Zollinger and R.E. Mandrell, 1983, Med. Trop. 43:143-147), eliciting protective antibodies (E. Wedege and L.O. Froholm, 1986, Infect. Immun. 51: 571-578; K. Saukkonen et al, 1987, Microb. Pathogen. 3:261-267), that give it a special importance in vaccine preparations.

Some subtypes of proteins P1 have been cloned in *E. coli*, starting from genomic libraries (A.K. Barlow et al., 1989, Molec. Microb. 3:131-139) or using the PCR technique (S. Butcher et al., VIIth International Congress of Neisseria, R.C. Seid, Patent Application WO 90/06696; Brian Mc Guinness et al., 1990, J. Exp. Med. 171:1871-1882, M.C.J. Maiden et al., VIIth International Conference of Neisseria, Berlin, Sept. 9-14, 1990, and 1991, Molec. Microb. 3:727; J. Suker et al., VIIth International Conference of Neisseria, Berlin, Sept. 9-14, 1990). However, up to now, there is no genetic construction able to produce this protein with 35 high levels of expression. Only low levels of expression (D.A. White et al., 1990, Molec. Microb. 4:769-776) or its expression in *Bacillus subtilis* fused to the outer membrane protein A of *E. coli* (omp A) (E. Wahlstrom et al., VIIth International Congress of Neisseria, September 9-14, 1990, Berlin) have been reported.

It can be affirmed that up to the moment no antigen has been isolated which is common to all types and serogroups of *N. meningitidis* and is able to produce bactericidal antibodies. For this reason, an antigen of this kind, conjugated or fused to other proteins or polysaccharides of immunological interest, would be 40 relevant as a candidate for bivalent vaccine preparations.

This invention is related to a nucleotide sequence coding for a protein having a molecular weight of about 64 kilodaltons. This sequence has been found in all *N. meningitidis* serotypes and serogroups tested, as verified by nucleic acid hybridization, Western-blotting, Dot-blot and ELISA.

45 A technical object of this invention is the identification of a nucleotide sequence which codes for a highly conserved protein and is common to the majority of pathogenic strains of *Neisseria* (named P64k), in order to obtain the protein by a recombinant way with a high grade of purity and in commercially useful quantities, so that it can be employed in diagnostic methods and as an integrating part of a vaccine preparation of broad spectrum of protection.

50 On the level of genetic information (DNA and RNA), the invention provides a recombinant polynucleotide, comprising a nucleotide sequence coding for a protein P64k of *Neisseria meningitidis*, said protein P64k essentially having the amino acid sequence shown in SEQ ID NO:1. In a preferred embodiment said nucleotide sequence coding for the protein P64k of *N. meningitidis* essentially consists of the nucleotide sequence shown in SEQ ID NO:1. The recombinant polynucleotide may further comprise a 55 nucleotide sequence of a cloning or expression vector.

The invention also provides a transformed microorganism containing a recombinant polynucleotide as defined above, preferably a transformed microorganism which is capable of expressing the protein P64k of *N. meningitidis*. In a particularly preferred embodiment of the invention, the transformed microorganism is

an *Escherichia coli* strain, e.g. *E. coli* strain HB101, transformed with an expression vector containing a nucleotide sequence coding for the protein P64k of *N. meningitidis*, e.g. the expression vector pM-6.

The invention also provides a recombinant proteinaceous substance, comprising an amino acid sequence corresponding to the amino acid sequence of at least a part of a protein P64k of *N. meningitidis*, said protein P64k essentially having the amino acid sequence shown in SEQ ID NO:1. Said recombinant proteinaceous substance may essentially consist of protein P64k, or be a fusion protein or a protein/polysaccharide conjugate comprising the amino acid sequence of protein P64k of *N. meningitidis*.

The invention further provides a vaccine composition, comprising a recombinant protein as defined above, together with a suitable carrier, diluent or adjuvant. A particular embodiment of this invention provides a vaccine composition, comprising a lipoamide dehydrogenase or acetyl transferase capable of inducing antibodies which can bind a protein P64k of *N. meningitidis*, together with a suitable carrier, diluent or adjuvant.

In addition, the invention provides a monoclonal antibody, raised against a recombinant proteinaceous substance as defined above, or against a lipoamide dehydrogenase or acetyl transferase, and capable of binding a protein P64k of *N. meningitidis*.

The invention also provides a process for preparing a protein P64k of *Neisseria meningitidis*, or a fusion protein comprising protein P64k, said protein P64k essentially having the amino acid sequence shown in SEQ ID NO:1, comprising the steps of transforming a microorganism with an expression vector containing a nucleotide sequence coding for said protein P64k, or said fusion protein, culturing the transformed microorganism to obtain expression of said protein P64k, or said fusion protein, and isolating said expression product.

One novel aspect of this invention is the gene isolated from the *N. meningitidis* strain B:4:P1.15, which was named M-6 and has as a principal characteristic its stability in *E. coli* vectors. This gene does not produce adverse effects on the host, allowing to obtain yields of over 25 % of total protein (ratio of P64k to total protein from host strain). On the other hand, it has been demonstrated by Southern and Western Blot hybridizations (E. Southern, 1975, *J. Mol. Biol.* 98: 503-527 and W. Burnette, 1981, *Anal. Biochem.* 12: 195-203) that protein P64k is present in all the following studied strains of *N. meningitidis*:

*N. meningitidis* A

*N. meningitidis* B:1

*N. meningitidis* B:2

*N. meningitidis* B:4

*N. meningitidis* B:5

*N. meningitidis* B:8

*N. meningitidis* B:9

*N. meningitidis* B:11

*N. meningitidis* B:15

*N. meningitidis* B:4:P1.15

*N. meningitidis* C

*N. meningitidis* B:15:P1.16

*N. meningitidis* B:15:P1.16 (H 44/76)

*N. meningitidis* B:NT (121/85)

*N. meningitidis* B:NT (71/86)

*N. meningitidis* B:NT (210/86)

and also in *N. mucosa*, *N. subflava* and *N. gonorrhoeae*.

The protein is not present in *N. cinerea*, *N. lactamica*, *N. sicca* and *N. flavescens*, but these are not of interest because they are not pathogenic.

The protein having a molecular weight of about 64 kDa can be localized by electron microscopy in the outer membrane of *N. meningitidis*. Therefore, this antigen is an exposed antigen which is favorable for use in a vaccine preparation. The protein was recognized in Western blot immunoidentification experiments with sera from convalescents and individuals vaccinated with the conventional Cuban vaccine Va-Mengoc-BC (Centro Nacional de Biopreparados, Havana, Cuba). This aspect guarantees the immunogenicity of the antigen and at the same time confirms its presence within the high molecular weight protein fraction constituent of this vaccine, which is responsible of the lasting immune response to the disease.

Another novel aspect is that the protein, which is an object of this invention, produces antibodies with a broad bactericidal spectrum (different serogroups, serotypes and subtypes), a characteristic which has not been reported previously for any protein from *N. meningitidis*.

This protein obtained in high levels in *E. coli* becomes an important candidate for the improvement of immunogenicity when expressed as a fusion protein with other proteins. It could also increase the

expression by conferring enhanced stability and suitability in the molecular structure during transcription and translation processes. Belonging to *Neisseria*, this protein can also be fused to other proteins from *Neisseria* in order to obtain vaccine preparations against this microorganism with increased immunogenicity. These fusion proteins are also objects of this invention.

On the other hand, surprisingly, it was found that the gene M-6 obtained from a genomic library of the strain *N. meningitidis* B:4:P1.15 showed a great homology with sequences of lipoamide-dehydrogenases and acetyl-transferases from other microorganisms and higher organisms. The presence of common antigenic determinants allows the use of these other related proteins as immunogens, able to confer protection by the induction of bactericidal antibodies which recognize the antigenic determinants common to protein P64k. Therefore, the use of these lipoamide-dehydrogenases and acetyl-transferases (not isolated from *N. meningitidis*) or derivatives therefrom such as peptides, fragments from enzymatic degradation, constructions of fusion with other proteins, or conjugation with proteins, polysaccharides or lipids, or insertion in complexes as liposomes or vesicles, etc., for vaccine purposes, are included in the scope of this invention.

An important object of this invention is the nucleotide sequence which codes for the M-6 gene (SEQ ID NO:1 of the Sequence Listing) whose product is the protein P64k.

This gene was derived from the genome of the strain B385 isolated in Cuba (*N. meningitidis* B:4:P1.15), by the construction of a genomic library in the phage EMBL 3.

The recombinant DNA including the gene M-6 constitutes another object of this invention, which includes the phage lambda, the plasmid pM-3 and the expression vector pM-6 for expression in bacteria.

In particular, for the intracellular expression in *E. coli*, the M-6 gene was cloned under the tryptophane promoter and using its own termination signal of transcription and a linkage fragment between M-6 and the cloning site NcoI which adds the following nucleotide sequence at the 5' end:

ATG CTA GAT AAA AGA (SEQ ID NO:2)

The N-terminal of the protein P64k encoded by the M-6 gene inserted in plasmid pM-6 which adds 5 aminoacids to the N-terminal of the original protein corresponds to:

M L D K R M A L V E L K V P D I G G H E N V D I I (SEQ ID NO:3)

Another object of this invention are the microorganisms resulting from the transformation of *E. coli* strain HB 101 with the pM-6 vector, which are characterized by the expression of high levels of protein P64k, good viability and great stability.

The transformed clone of *E. coli* was denominated HBM64 (Fig. 2), and presents levels of expression of P64k higher than 25 % in relation to the total protein of the cell (Fig. 6).

The procedure described in the present invention, due to the levels of expression achieved for this product, allows to reach an optimal purity for use of this protein in humans.

On the other hand, the antigen obtained from the isolated sequence was very useful in the preparation of different types of potential vaccine preparations, like bivalent vaccines with a broad immunoprotective spectrum, e.g., protein-polysaccharide conjugates, fusion proteins, etc.

EXAMPLES: These examples intend to illustrate the invention, but not to limit the scope of this invention.

#### EXAMPLE 1:

For the isolation of genomic DNA from *N. meningitidis* B:4:P1.15, the cells were grown in Mueller-Hinton medium (OXOID, London). The biomass from a culture of 100 ml was resuspended in 8 ml of Tris (hydroxymethyl-aminomethane) 100 mM, EDTA (ethylenediamine tetraacetic acid) 1mM, pH 8. The cells were subjected to a treatment with lysozyme (10 mg/ml), followed by 200  $\mu$ l of self-digested pronase (20 mg/ml) and 1.1 ml of 10% SDS. The mixture was incubated at 37 ° C during 1 hour, then it was treated with phenolchloroform (v/v) and the remains of phenol were eliminated using 2-butanol. Finally, the DNA was precipitated with absolute ethanol and RNA was eliminated with ribonuclease A (Sigma, London).

The DNA of about 60 kb was subjected to a partial digestion with the enzyme *Sau* 3A, obtaining a population of fragments of about 15 kb. This majoritary fraction was isolated and purified by separation in agarose gel (T. Maniatis et al., 1982, Molecular Cloning: A Laboratory Manual. Cold Spring Harbor Lab.: Cold Spring Harbor NY).

For the construction of the genomic library, the process described by Maniatis was essentially followed (T. Maniatis et al., 1982, Molecular Cloning: A Laboratory Manual. Cold Spring Harbor Lab.: Cold Spring Harbor NY). Four  $\mu$ g of purified DNA were ligated with 8  $\mu$ g of BamHI-digested EMBL-3. The ligation product was packed and the phages were finally plated on the *E. coli* strain C66P2.

The library was screened by immunoidentification (R. Young and R. Davis, 1983, PNAS USA 80: 1194-



1198) using rabbit serum obtained against a preparation of proteins belonging to the outer membrane of the strain *N. meningitidis* B:4:P1.15. The clones were analyzed by Western-blot (Burnette, 1981) and the expression of the P64k protein with a molecular weight of about 70 kDa was detected. The resulting recombinant phage was named 31. The Western blot was also made using a mixture of sera from

This experiment was repeated using sera from several healthy individuals, and the signal obtained was negative against the recombinant protein P64k.

#### EXAMPLE 2:

For subcloning in bacteria, the 17 kb insert corresponding to the phage isolated from the library was cloned in the plasmid pUC18 after separation from the phage's arms using the enzyme *Sall*. This resulted in the construction pM-1 (Fig. 2), that was subjected to restriction analysis (Fig. 3).

The fragment *Sall*-*HindIII* of about 6 kb was recloned in the plasmid pUC18 and the construction pM-2 was obtained (Fig. 2). In order to obtain a more exact localization of the gene coding for protein P64k deletions were carried out with the enzymes *ClaI*, *EcoRI* and *HincII*. The complete fragment of the gene M-6 was finally localized as an *EcoRI*-*HindIII* insert corresponding to the construction pM-3 (Fig. 2).

In all constructions, the presence of the gene was confirmed by recognizing the protein by colony immunoidentification and Western Blot using hyperimmunized rabbit sera.

The sequence of the insert in pM-3 was determined by the method of Sanger (F. Sanger et al., 1977, PNAS USA 74: 5463-5467).

From the obtained sequence, the approximate molecular weight of the protein encoded by the gene was deduced.

In order to obtain a construction for high expression of the protein P64k, the plasmid pM-3 (Fig. 2) was linearized with the enzyme *EcoRI* and successive suppressions of the gene were carried out, incubating the sample with the nucleases *ExoIII* and *S1*.

The resulting fragments were separated from the rest of the vector pUC18 by cutting with the restriction enzyme *HindIII* and were cloned fused to a stabilizer fragment (European patent application EP-A-0 416 673), using an *Xba*-blunt adapter to conserve the *XbaI* site of the stabilizer gene:

5' C T A G A T A A A G A 3' (SEQ ID NO:4)

3' T A T T T T C T 5' (SEQ ID NO:5)

The constructions in which the fused fragment coincided with the reading frame were selected by immunoidentification using hyperimmune rabbit sera.

The insert sequences were established using Sanger's Method (F. Sanger et al., 1977, PNAS USA 74: 5463-5467). From the obtained sequences the approximate molecular weight of the protein encoded by this gene was deduced.

The fusion region between the proteins was localized in the gene sequences. In the clone pILM-25 (Figure 4) the ATG of the gene predetermined by the sequence of the DNA insert isolated from the library, coincided with the fusion site.

The *NcoI*-*XbaI* fragment, corresponding to the stabilizing peptide coding sequence, was deleted from pILM-25, obtaining a non-fused protein expressed under the tryptophan promoter with its original terminator from the *N. Meningitidis* B:4:P1.15, according to the pM-6 construction (Figure 1).

The pM-6 plasmid was transformed in different strains of *E. coli* like W3110, JA-221, HB-101, LE-392 and MC-1061, and the expression of P64k was compared. The best results were obtained in W3110, JA-221 and HB-101. These strains were chosen to scale up fermentation, and expression levels up to 25 % of total cell proteins were obtained.

#### EXAMPLE 3:

To confirm the correct expression of the cloned gene the N-terminal region of the intact protein was subjected to the Edman degradation method (P. Edman, 1950, Acta Chem. Scand. 4: 283-293). This

technique elucidates the sequence (primary structure) of this region in the molecule.

The P64k protein was desalted by gel filtration chromatography (PD-10, Pharmacia), eluted with water and monitored at 280 nm. The protein fraction was concentrated to 0.5 nM/ $\mu$ l. One  $\mu$ l of this solution was applied to a PVDF (polyvinylidene difluoride, Millipore) filter, previously activated with methanol.

5 The Edman degradation was made using the Knauer's Automatic Sequencer, model 810, connected to a HPLC (High Performance Liquid Chromatography) system, so as to detect the phenylthiohydantoin derivatives of the aminoacids (PTH-aminoacids). The standard procedure of sequencing as recommended by the manufacturer of the equipment was followed. The separation of the PTH-aminoacids was performed in a reverse phase column C-18 (5  $\mu$ m), 250 mm x 2 mm (Merck), eluted with an acetonitrile gradient (B  
10 buffer) in sodium acetate (A buffer), prepared according to the manufacturers, with a 200  $\mu$ l/minute flow and at 42° C. The PTH-aminoacids were detected at 269 nm.

Data processing and registration were made in a Shimadzu model CR-6a automatic integrator, using a program for data processing by subtraction of two consecutive chromatograms, to facilitate the evaluation of the Edman degradation cycles. Sequence identification is obtained by the chromatographic evaluation of the  
15 corresponding analyzed cycle and confirmed by the chromatogram obtained by subtraction, allowing to determine 25 residues.

#### EXAMPLE 4:

20 To demonstrate that the protein P64k is recognized by the sera of individuals vaccinated with the Cuban Va-Mengoc-BC preparation (Centro Nacional de Biopreparados, Havana, Cuba.), a Western-Blot was made, with a mixture of 12 sera from adults (immunized with two doses of the Cuban vaccine) diluted in a solution containing defatted milk (Oxoid, London). The experiment included:  
recombinant protein P64k, purified from E. coli HB-101 transformed with the pM-6 plasmid;  
25 supernatant of the ultrasonic cell rupture of untransformed E. coli HB-101;  
the reaction was revealed with a protein A-colloidal gold conjugate.  
It was shown that the protein P64k is recognized by the pool of sera.

#### EXAMPLE 5:

30 The bactericidal test against B385 (B:4:P1.15) was made according to the procedure described by Larrick et al. (Scand. J. Immunol. 32, 1990, 121-128) with modifications. With this objective, a mixture was made of a) a suspension of bacteria, cultured under special conditions (1-5 colony forming units/1), b) Gey's balanced salt solution, c) rabbit sera (3 to 4 weeks) as a source of complement and d) pooled sera from  
35 mice, immunized against protein P64k in Aluminium Hydroxyde Gel, and inactivated at 56° C for 30 minutes. The immunization of mice was carried out according to an immunization scheme of 3 doses of 20  $\mu$ g each. The proportions used in the aforementioned mixture were 1:2:1:1 in a total volume of 125  $\mu$ l. The mixture was incubated at 37° C during 1 hour and plated in fresh Mueller Hinton Agar (Oxoid, London) supplemented with 5 % calf serum (CubaVet, Habana). The counting of surviving colonies was done after  
40 18 hours of incubation of the plates in an atmosphere of 5 % CO<sub>2</sub> at 37° C.

The bactericidal titer was considered as the maximum serum dilution necessary to render a 50 % inhibition of bacterial growth, with respect to the same mixture without the test serum. It was found that 1:20 serum dilution still maintains its bactericidal activity. As negative controls (non bactericidal at 1:2 dilution) pooled sera from mice immunized with Aluminum Hydroxyde Gel, and pooled sera from mice immunized  
45 with cuban Hepatitis B recombinant vaccine, were used. The bactericidal effect was specific to the anti-P64k antibodies.

#### EXAMPLE 6:

50 The bactericidal test against different strains of N. meningitidis was made using:  
1. An ammonium sulphate precipitate of the supernatant harvested from a culture of hybridoma cells secreting monoclonal antibodies specific against P64k (anti P64k)/Sample to analyze.  
2. An ammonium sulphate precipitate of the supernatant harvested from hybridoma cells secreting monoclonal antibodies specific against the P1.15 protein present in N. meningitidis strain B385 (anti  
55 P1.15)/Positive control of the system.

The maximum dilutions tested were always 1:16. The maximum dilutions tested which had a bactericidal effect, according to the EXAMPLE 5, are indicated:

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Strain	anti-P64k	anti-P1.15
B385	1:16	1:16
B:4:P1.15	1:16	1:16
B:14:P1.7	1:16	-
B:NT:NT	1:16	-
B:15:P1.15	1:8	-
B:15:P1.16	1:8	-
B:13	1:8	-
C	1:16	-
A	1:16	-

As seen, the anti-P64k monoclonal antibodies have significant bactericidal titers against different serogroups (A, B and C), serotypes (4, 14, 13, 15 and NT) and subtypes (7, 15, 16 and NT) of bacteria.

## EXAMPLE 7:

Fusion protein M-14 (P64k and P1.15)

In order to obtain a genetic construction for high expression that contained the variable epitopes of the P1.15 protein (Outer membrane protein from *N. meningitidis* B:4:P1.15) fused to the P64k protein, the gene coding for P1.15 protein was cloned using the Polymerase Chain Reaction (PCR). The following region containing the variable immunodeterminants of P1.15:

```

L Q L T E P P S K S Q P Q V K V T K A K S R I R T K I S D F G
S F I G F K G S E D L G E G L K A V W Q L E Q D V S V A G G G
A T Q W G N R E S F V G L A G E F G T L R A G R V A N Q F D D
A S Q A I D P W D S N N D V A S Q L G I F K R H D D M P V S V
R Y D S P D F S G F S G S V Q F V P I Q N S K S A Y T P A Y H
Y T R Q N N A D V F V P A V V G K P G S D V Y V A G L N Y K N
G G F A G S Y A F K Y A R H A N V G R N A F E L F L L G S T S
D E A

```

(SEQ ID NO:6)

was inserted in the Mlu I site of the gene M-6, encoding for P64k, after having been made blunt with the klenow fragment from DNA polymerase I. The sites for gene fusion of P1.15 with M-6 are the following:

GDALQL

(SEQ ID NO:7)

```

      Gly Asp Ala   Leu Gln Leu
5'-  GGC GAC GCG   CTG CAG TTGA   -3'   (SEQ ID NO:8)
      M-6                P1.15

```

EANAYE

(SEQ ID NO:9)

5

Glu Ala Asn\*Ala Tyr Glu

5'- GAA GCC AAC GCG TAC GAA -3' (SEQ ID NO:10)

P1.15

M-6

10

\*: N does not belong to any of the fusion proteins and was created by the genetic construction.

15

The resulting fusion protein (M-14) was expressed in *E. coli* using a plasmid vector under the tryptophan promoter, to levels higher than 10 % of total cell protein. The protein was recognized by bactericidal monoclonal antibodies, and anti-P1.15 and P64k polyclonal antibodies, in Western-Blot.

## 20 EXAMPLE 8:

Polysaccharide/P64k conjugation.

The protein P64k was conjugated with the polysaccharide from *Haemophilus influenzae* using the reductive amination method. The *Haemophilus influenzae* polysaccharide (Polyribosyl ribitol phosphate, PRP) was purified by the cold phenol method described by Frasch, 1990 (in: *Bacterial Vaccines*, 1990, Alan R. Liss, Inc., pp. 123-145). The final contamination of PRP with proteins or nucleic acids was less than 1 %. This polysaccharide was degraded using the method of Parikh et al. 1974 (*Methods in Enzymol.* 34B: 77-102) with sodium periodate in PRP (ratio 1 : 5 w/w) dissolved in 0.1 M sodium acetate (pH 4.5). The incubation was carried out in the dark during 30 minutes with stirring. The periodate excess was eliminated by addition of ribitol. Very low molecular weight compounds were eliminated by dialysis (Medicell International Ltd. Membrane, London). The resulting oligosaccharide had free aldehyde groups able to react with primary amines (e.g. lysine residues in proteins). The conjugate is obtained by mixing protein and polysaccharide in a 1 : 1 ratio (w/w), adding sodium cyanoborohydride and subjecting the mixture to an incubation, first for 48 hours at 4°C and later at 37°C for 24 hours. The high molecular weight complex which contains the resulting conjugate with protein-polysaccharide in a 1 : 2.3 ratio, can be separated from the non reactive contaminants by HPLC.

## 40 EXAMPLE 9:

Bivalent vaccine preparation against Hepatitis B virus and *N. meningitidis*.

In order to obtain a bivalent vaccine preparation, different quantities of protein P64k and Hepatitis B Surface Antigen (Vacuna Recombinante contra 1a Hepatitis B, Heber Biotec, Havana, Cuba) were mixed. The antigens were adjuvated with Aluminum Hydroxyde Gel, at 2mg/dose and inoculated in Balb/c mice having a body weight of 20 g in 3 dosis of 0.5 ml each. Different variants were assayed:

1. P64k 20 µg (P20)
2. HBsAg 20 µg (H20)
3. P64k 10 µg + HBsAg 10 µg (P10:H10)
4. P64K 15 µg + HBsAg 5 µg (P15:H5)
- 50 5. Placebo (Al(OH)<sub>3</sub>)

Seven days after the immunization with the first doses, the second doses were applied. The third dose was given 14 days after the second. Seven days later, blood was taken and the serum of each immunized animal was separated. Antibody titers against P64k protein were measured in solid phase Enzyme Linked Immunosorbent Assay (ELISA), using P64k at 5 mg/ml to coat the polystyrene plate. The antibody titers against HBsAg were determined by a Commercial ELISA (Organon Teknika, Boxtel). Figure 5 shows the dynamics of antibody response against protein P64k, using sera diluted 1/10 000. The response against P64k is not interfered by the presence of the other antigen. Figure 6 shows the titers against HBsAg after each dosis. The titers against this protein are not diminished by the presence of P64k in the preparation.

High titers are obtained against both antigens in the same vaccine preparation.

EXAMPLE 10:

A software was created to search the EMBL (European Molecular Biology Laboratory) Data Base and detect the homology between P64k and other proteins. As result of the search it was found that there is homology of one segment in the sequence of P64k with segments in the sequences of *N. gonorrhoeae*. This sequence was found as characteristic in both *N. gonorrhoeae* and *N. meningitidis* (F.F. Correia, S. Inouye and M. Inouye, 1988, J. Biol. Chem. 263, No. 25, 12194-12198).

Another region with high homology was found in two proteins of the Pyruvate Dehydrogenase Complex from *E. coli* K12:

a) Acetyltransferase from *E. coli* and the P64k outer membrane protein from *N. meningitidis*.

Homology exists between a segment comprising 100 amino acids, repeated at the beginning of the amino acid sequence of the Acetyltransferase ("Lipoyl Domain", including the "Lipoyl Binding Site" (P.E. Stephens et al., 1983, Eur. J. Biochem. 133, 481-489)) and a region located in the first 111 amino acids of the P64k:

```
MALVELKVPDIGGHENVNDIIAVEVNVGDTIAV      (SEQ ID NO:11)
- *- ***** - *-- * * * * - *
VKEVNVPDIGG DEVEVTEVMVKVGDKVAA          (SEQ ID NO:12)
```

```
DDTLITLETDKATMDVPAEVAGVVKEVKVKVG      (SEQ ID NO:11) (cont)
-- ***-* * * * *-*** *****-* * *
EQSLITVEGDKASMEVPAPFAGVVKELKVNVG      (SEQ ID NO:12) (cont)
```

```
DKISEGGLIVVVEAEGT--AAAPKAESAA--A      (SEQ ID NO:11) (cont)
** - * * *- * * * * * * * - * * *
DKVKTGSLIMIFEVEGAAPAAAPAKQEAAAPA      (SEQ ID NO:12) (cont)
```

```
PRKKPLKCRWVPQAAQFGG                      (SEQ ID NO:11) (cont)
* * * * *
PAAKAEAPAAAPAAKAEKG                      (SEQ ID NO:12) (cont)
```

where (\*) indicates positions with the same amino acids and (-) indicates positions of conservative amino acid changes.

b) Lipoamide Dehydrogenase from *E. coli* and Outer Membrane P64k protein from *N. meningitidis*.

Homology exists between the Lipoamide Dehydrogenase from *E. coli* (a protein having 473 amino acids, P.E. Stephens et al., 1983, Eur. J. Biochem. 133, 481-489) and the protein P64k, specifically in a segment which represents almost the total protein, except the region with homology with the "lipoyl domain" from Acetyltransferase.

	---1---	
	SADAEYDVVVLGGPGGYSAFAAADEGLKVA	(SEQ ID NO:13)
5	STEIKTQVVVLGAGPAGYSAAFRCADLGLETV	(SEQ ID NO:14)
	-----2-----	
10	IVERYKTLGGVCLNVGCIPSKALLHNAVIDE	(SEQ ID NO:13) (cont)
	IVERYNTLGGVCLNVGCIPSKALLHVAKVIEE	(SEQ ID NO:14) (cont)
15	VRHLAANGIKYPEPALDIDMLRAYKDGVSRL	(SEQ ID NO:13) (cont)
	AKALAEHGIVFGEPKTDIDKI TWKEKVINQL	(SEQ ID NO:14) (cont)
20	TG-FGRYGEKRKVDVIQGDGQFLDPHHLEVSL	(SEQ ID NO:13) (cont)
	TGGLAGMAKGRKVKVNGLGKFTGANTLEVEG	(SEQ ID NO:14) (cont)
25	TAGDAYEQAAPTGEKKIVAFKNCIIAAGSRVT	(SEQ ID NO:13) (cont)
	ENG-----KTVINFDNAIIAAGSRPI	(SEQ ID NO:14) (cont)
30	KLPFIP-EDPRIIDSSGALALKEVPGKLLIIG	(SEQ ID NO:13) (cont)
	QLPFIPHEDPRIWDSTDALELKEVPERLLVMG	(SEQ ID NO:14) (cont)
35	GGIIGLEMGTVYSTLGSRLDVVEMMDGLMQGA	(SEQ ID NO:13) (cont)
	GGIIGLEMGTVYHALGSQIDVVEMFDQVIPAA	(SEQ ID NO:14) (cont)
40	DRDLVKVWQKQNEYRFDNIMVNTKTVAVEPKE	(SEQ ID NO:13) (cont)
	DKDIVKVFTKRISKKN-LMLETKVTAVEAKE	(SEQ ID NO:14) (cont)
45	DGVYVTFEGANPPKEPQRYDAVLVAAGRPNP	(SEQ ID NO:13) (cont)
	DGIYVTMEGKKAPAEQRYDAVLVAIGRVPNG	(SEQ ID NO:14) (cont)
50	KLISAEKAGVAVTDRGFIEVDKQMRITNVPHIY	(SEQ ID NO:13) (cont)
	KNLDAGKAGVEVDDRGRFIRVDKQLRTNVPHIF	(SEQ ID NO:14) (cont)

AIGDIVGQPM LAHKAVHEGHVAAENCAGTKAY (SEQ ID NO:13) (cont)

\*\*\*\*\*-\*\*\*\*\* \*\*-\* \*

AIGDIVGOPMLAHKGVHEGHVAAEVIAGKKHY (SEQ ID NO:14) (cont)

FDAAVIPGVAYTSPEVAWVGETELSAKRPAGK (SEQ ID NO:13) (cont)

\*\*\*-\*\*\*-\*\*\*-\*\*\*\*\* \*\* -\*\* -

FDPKVIPSIAYTEPEVAWVGLTEKEAKEKGIS (SEQ ID NO:14) (cont)

ITKANFPWAASGRAIANGCDKPF TKLIFDAET (SEQ ID NO:13) (cont)

\*-\*\*\*\*\*--\*-- --\*\*\*\*\* \*-

YETATFPWAASGRAIASDCADGMTKLIFDKES (SEQ ID NO:14) (cont)

GRIIGGGIVGPNGGDMIAKSALPSKLGCDAAAD (SEQ ID NO:13) (cont)

\*-\*\*\*-\*\*\*-\*\*\*- - - - - \* - - - - \*\*\*-\*

HRVIGGAIVGTNGGELLGEIGLAIEMGCDAED (SEQ ID NO:14) (cont)

|--3-|  
VGKTIHPRPTLGESIGMAAEVALGTCTDLPPQ (SEQ ID NO:13) (cont)

\*\*\*--\*\*\* \*\*-\*-\*\*\*\* \*--\*\*\*\*

IALTIHAHPTLHESVGLAAEVFEGSITDLPNP (SEO ID NO:14) (cont)

--KKK - MEN1pd (SEQ ID NO:13) (cont)

\*\*\*

KAKKK - EC1pd (SEQ ID NO:14) (cont)

Where:

[-1-]: Adenine binding site (FAD)

[-2-]: Redox active disulphide region

[-3-]: Active site histidine

Strain deposits:

An *E. coli* HB-101 clone containing the plasmid pM-3 (a pUC18 plasmid containing the 4.1 kb DNA fragment from *Neisseria meningitidis*, strain B:4:P1.15, cloned between the EcoRI and HindIII restriction sites), was deposited on August 30, 1991, with the Centraalbureau voor Schimmelcultures (CBS), Baarn, The Netherlands, and obtained deposit number CBS 485 .91.

## SEQUENCE LISTING

5

SEQ ID NO:1

SEQUENCE TYPE : Nucleotide with corresponding amino acid

10

SEQUENCE LENGTH: 1830 bp

STRANDEDNESS: Single

TOPOLOGY: Linear

15

MOLECULE TYPE: genomic DNA

ORIGINAL SOURCE ORGANISM: N. meningitidis group B

IMMEDIATE EXPERIMENTAL SOURCE: Strain B:4:P1:15 isolated in  
Cuba

20

FEATURES: From 1 to 1830 bp mature protein

PROPERTIES: Gene coding for P64k protein from outer membrane  
of N. meningitidis

25

ATG	CTA	GAT	AAA	AGA	ATG	GCT	TTA	GTT	GAA	TTG	AAA	GTG	CCC	42
Met	Leu	Asp	Lys	Arg	Met	Ala	Leu	Val	Glu	Leu	Lys	Val	Pro	
1				5					10					

30

GAC	ATT	GGC	GGA	CAC	GAA	AAT	GTA	GAT	ATT	ATC	GCG	GTT	GAA	84
Asp	Ile	Gly	Gly	His	Glu	Asn	Val	Asp	Ile	Ile	Ala	Val	Glu	
15					20					25				

35

GTA	AAC	GTG	GGC	GAC	ACT	ATT	GCT	GTG	GAC	GAT	ACC	CTG	ATT	126
Val	Asn	Val	Gly	Asp	Thr	Ile	Ala	Val	Asp	Asp	Thr	Leu	Ile	
	30					35					40			

40

ACT	TTG	GAA	ACC	GAT	AAA	GCG	ACT	ATG	GAC	GTA	CCT	GCT	GAA	168
Thr	Leu	Glu	Thr	Asp	Lys	Ala	Thr	Met	Asp	Val	Pro	Ala	Glu	
		45					50					55		

45

GTT	GCA	GGC	GTA	GTC	AAA	GAA	GTT	AAA	GTT	AAA	GTC	GGC	GAC	210
Val	Ala	Gly	Val	Val	Lys	Glu	Val	Lys	Val	Lys	Val	Gly	Asp	
			60					65					70	

50

AAA	ATC	TCT	GAA	GGT	GGT	TTG	ATT	GTC	GTC	GTT	GAA	GCT	GAA	252
Lys	Ile	Ser	Glu	Gly	Gly	Leu	Ile	Val	Val	Val	Glu	Ala	Glu	
				75					80					

55

GGC	ACG	GCA	GCC	GCT	CCT	AAA	GCC	GAA	TCG	GCT	GCC	GCC	CCG	294
Gly	Thr	Ala	Ala	Ala	Pro	Lys	Ala	Glu	Ser	Ala	Ala	Ala	Pro	
85					90					95				



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	CGC	AAG	AAG	CCC	CTA	AAC	GTG	CCG	CTC	CCT	GCT	CCG	CAA	GCC	336
	Arg	Lys	Lys	Pro	Leu	Asn	Val	Pro	Leu	Pro	Ala	Pro	Gln	Ala	
		100					105					110			
5	GCG	CAA	TTC	GGC	GGT	TCT	GCC	GAT	GCC	GAG	TAC	GAT	GTG	GTC	378
	Ala	Gln	Phe	Gly	Gly	Ser	Ala	Asp	Ala	Glu	Tyr	Asp	Val	Val	
			115					120					125		
10	GTA	TTG	GGT	GGC	GGT	CCC	GGC	GGT	TAC	TCC	GCT	GCA	TTT	GCC	420
	Val	Leu	Gly	Gly	Gly	Pro	Gly	Gly	Tyr	Ser	Ala	Ala	Phe	Ala	
				130					135					140	
15	GCT	GCC	GAT	GAA	GGC	TTG	AAA	GTC	GCC	ATC	GTC	GAA	CGT	TAC	462
	Ala	Ala	Asp	Glu	Gly	Leu	Lys	Val	Ala	Ile	Val	Glu	Arg	Tyr	
					145					150					
20	AAA	ACT	TTG	GGC	GGC	GTT	TGC	CTG	AAC	GTC	GGC	TGT	ATC	CCT	504
	Lys	Thr	Leu	Gly	Gly	Val	Cys	Leu	Asn	Val	Gly	Cys	Ile	Pro	
	155					160					165				
	TCC	AAA	GCC	TTG	TTG	CAC	AAT	GCC	GCC	GTT	ATC	GAC	GAA	GTG	546
	Ser	Lys	Ala	Leu	Leu	His	Asn	Ala	Ala	Val	Ile	Asp	Glu	Val	
		170					175					180			
25	CGC	CAC	TTG	GCT	GCC	AAC	GGT	ATC	AAA	TAC	CCC	GAG	CCG	GAA	588
	Arg	His	Leu	Ala	Ala	Asn	Gly	Ile	Lys	Tyr	Pro	Glu	Pro	Glu	
			185					190					195		
30	CTC	GAC	ATC	GAT	ATG	CTT	CGC	GCC	TAC	AAA	GAC	GGC	GTA	GTT	630
	Leu	Asp	Ile	Asp	Met	Leu	Arg	Ala	Tyr	Lys	Asp	Gly	Val	Val	
				200					205					210	
35	TCC	CGC	CTC	ACG	GGC	GGT	TTG	GCA	GGT	ATG	GCG	AAA	AGC	CGT	672
	Ser	Arg	Leu	Thr	Gly	Gly	Leu	Ala	Gly	Met	Ala	Lys	Ser	Arg	
					215					220					
40	AAA	GTG	GAC	GTT	ATC	CAA	GGC	GAC	GGG	CAA	TTC	TTA	GAT	CCG	714
	Lys	Val	Asp	Val	Ile	Gln	Gly	Asp	Gly	Gln	Phe	Leu	Asp	Pro	
	225					230					235				
	CAC	CAC	TTG	GAA	GTG	TCG	CTG	ACT	GCC	GGC	GAC	GCG	TAC	GAA	756
	His	His	Leu	Glu	Val	Ser	Leu	Thr	Ala	Gly	Asp	Ala	Tyr	Glu	
		240					245					250			
45	CAG	GCA	GCC	CCT	ACC	GGC	GAG	AAA	AAA	ATC	GTT	GCC	TTC	AAA	798
	Gln	Ala	Ala	Pro	Thr	Gly	Glu	Lys	Lys	Ile	Val	Ala	Phe	Lys	
			255					260					265		
50	AAC	TGT	ATC	ATT	GCA	GCA	GGC	AGC	CGC	GTA	ACC	AAA	CTG	CCT	840
	Asn	Cys	Ile	Ile	Ala	Ala	Gly	Ser	Arg	Val	Thr	Lys	Leu	Pro	
				270					275					280	

55

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	TTC	ATT	CCT	GAA	GAT	CCG	CGC	ATC	ATC	GAT	TCC	AGC	GGC	GCA	882
	Phe	Ile	Pro	Glu	Asp	Pro	Arg	Ile	Ile	Asp	Ser	Ser	Gly	Ala	
				285						290					
5	TTG	GCT	CTG	AAA	GAA	GTA	CCG	GGC	AAA	CTG	CTG	ATT	ATC	GGC	924
	Leu	Ala	Leu	Lys	Glu	Val	Pro	Gly	Lys	Leu	Leu	Ile	Ile	Gly	
	295					300					305				
10	GGC	GGC	ATT	ATC	GGC	CTC	GAG	ATG	GGT	ACG	GTT	TAC	AGC	ACG	966
	Gly	Gly	Ile	Ile	Gly	Leu	Glu	Met	Gly	Thr	Val	Tyr	Ser	Thr	
		310					315					320			
15	CTG	GGT	TCG	CGT	TTG	GAT	GTG	GTT	GAA	ATG	ATG	GAC	GGC	CTG	1008
	Leu	Gly	Ser	Arg	Leu	Asp	Val	Val	Glu	Met	Met	Asp	Gly	Leu	
			325					330					335		
20	ATG	CAA	GGC	GCA	GAC	CGC	GAT	TTG	GTA	AAA	GTA	TGG	CAA	AAA	1050
	Met	Gln	Gly	Ala	Asp	Arg	Asp	Leu	Val	Lys	Val	Trp	Gln	Lys	
				340					345					350	
25	CAA	AAC	GAA	TAC	CGT	TTT	GAC	AAC	ATT	ATG	GTC	AAC	ACC	AAA	1092
	Gln	Asn	Glu	Tyr	Arg	Phe	Asp	Asn	Ile	Met	Val	Asn	Thr	Lys	
					355					360					
30	ACC	GTT	GCA	GTT	GAG	CCG	AAA	GAA	GAC	GGC	GTT	TAC	GTT	ACC	1134
	Thr	Val	Ala	Val	Glu	Pro	Lys	Glu	Asp	Gly	Val	Tyr	Val	Thr	
	365					370					375				
35	TTT	GAA	GGC	GCG	AAC	GCC	CCT	AAA	GAG	CCG	CAA	CGC	TAC	GAT	1176
	Phe	Glu	Gly	Ala	Asn	Ala	Pro	Lys	Glu	Pro	Gln	Arg	Tyr	Asp	
		380					385					390			
40	GCC	GTA	TTG	GTT	GCC	GCC	GGC	CGC	GCG	CCC	AAC	GGC	AAA	CTC	1218
	Ala	Val	Leu	Val	Ala	Ala	Gly	Arg	Ala	Pro	Asn	Gly	Lys	Leu	
			395					400					405		
45	ATC	AGC	GCG	GAA	AAA	GCA	GGC	GTT	GCC	GTA	ACC	GAT	CGC	GGC	1260
	Ile	Ser	Ala	Glu	Lys	Ala	Gly	Val	Ala	Val	Thr	Asp	Arg	Gly	
				410					415					420	
50	TTC	ATC	GAA	GTG	GAC	AAA	CAA	ATG	CGT	ACC	AAT	GTG	CCG	CAC	1302
	Phe	Ile	Glu	Val	Asp	Lys	Gln	Met	Arg	Thr	Asn	Val	Pro	His	
					425					430					
55	ATC	TAC	GCC	ATC	GGC	GAC	ATC	GTC	GGT	CAG	CCG	ATG	TTG	GCG	1344
	Ile	Tyr	Ala	Ile	Gly	Asp	Ile	Val	Gly	Gln	Pro	Met	Leu	Ala	
	435					440					445				
60	CAC	AAA	GCC	GTT	CAC	GAA	GGC	CAC	GTT	GCC	GCC	GAA	AAC	TGC	1386
	His	Lys	Ala	Val	His	Glu	Gly	His	Val	Ala	Ala	Glu	Asn	Cys	
		450					455					460			

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	GCC	GGC	AAC	AAA	GCC	TAC	TTC	GAC	GCA	CGG	GTG	ATT	CCG	GGC	1428
	Ala	Gly	Asn	Lys	Ala	Tyr	Phe	Asp	Ala	Arg	Val	Ile	Pro	Gly	
			465					470					475		
5	GTT	GCC	TAC	ACT	TCC	CCC	GAA	GTG	GCG	TGG	GTG	GGC	GAA	ACC	1470
	Val	Ala	Tyr	Thr	Ser	Pro	Glu	Val	Ala	Trp	Val	Gly	Glu	Thr	
				480					485					490	
10	GAA	CTG	TCC	GCC	AAA	GCC	TCC	GCG	CGC	AAA	ATC	ACC	AAA	GCC	1512
	Glu	Leu	Ser	Ala	Lys	Ala	Ser	Ala	Arg	Lys	Ile	Thr	Lys	Ala	
					495					500					
15	AAC	TTC	CCG	TGG	GCG	GCT	TCC	GGC	CGT	GCG	ATT	GCC	AAC	GGT	1554
	Asn	Phe	Pro	Trp	Ala	Ala	Ser	Gly	Arg	Ala	Ile	Ala	Asn	Gly	
	505					510					515				
20	TGC	GAC	AAG	CCG	TTT	ACC	AAG	CTG	ATT	TTT	GAT	GCC	GAA	ACC	1596
	Cys	Asp	Lys	Pro	Phe	Thr	Lys	Leu	Ile	Phe	Asp	Ala	Glu	Thr	
		520					525					530			
25	GGC	CGC	ATC	ATC	GGC	GGC	GGC	ATT	GTC	GGT	CCG	AAC	GGT	GGC	1638
	Gly	Arg	Ile	Ile	Gly	Gly	Gly	Ile	Val	Gly	Pro	Asn	Gly	Gly	
			535					540					545		
30	GAT	ATG	ATC	GCG	AAG	TCT	GCC	TTG	CCA	TCG	AAA	TGG	GCT	GCG	1680
	Asp	Met	Ile	Ala	Lys	Ser	Ala	Leu	Pro	Ser	Lys	Trp	Ala	Ala	
				550					555					560	
35	ACA	CGT	GCA	GAC	ATC	GGC	AAA	ACC	ATC	CAC	CCG	CGC	CCG	ACC	1722
	Thr	Arg	Ala	Asp	Ile	Gly	Lys	Thr	Ile	His	Pro	Arg	Pro	Thr	
					565					570					
40	TTG	GGC	GAA	TCC	ATC	GGT	ATG	GCG	GCG	GAA	GTG	GCA	TTG	GGT	1764
	Leu	Gly	Glu	Ser	Ile	Gly	Met	Ala	Ala	Glu	Val	Ala	Leu	Gly	
	575					580					585				
45	ACT	TGT	ACC	GAC	CTG	CCT	CCG	CAA	AAG	AAA	AAA	TAA			1800
	Thr	Cys	Thr	Asp	Leu	Pro	Pro	Gln	Lys	Lys	Lys	*			
		590					595				599				
50	ATCC	GACTGAATAA	ACAGCCGATA	AGGT	TTATTT	GA									1836
55	SEQ ID NO: 2														
	SEQUENCE TYPE : Nucleotide														
	SEQUENCE LENGTH: 15 bases														
50	ATGCTAGATA	AAAGA													15

SEQ ID NO: 3

SEQUENCE TYPE : Amino acid

SEQUENCE LENGTH: 25 amino acids

MOLECULE TYPE: Sequence N-terminal of P64k protein from outer  
membrane of *N. meningitidis*

Met	Leu	Asp	Lys	Arg	Met	Ala	Leu	Val	Glu	Leu	Lys	Val	Pro	Asp
1				5					10					15
Ile	Gly	Gly	His	Glu	Asn	Val	Asp	Ile	Ile					
				20					25					

SEQ ID NO: 4

SEQUENCE TYPE : Nucleotide

SEQUENCE LENGTH: 12 bases

CTAGATAAAA GA 12

SEQ ID NO: 5

SEQUENCE TYPE : Nucleotide

SEQUENCE LENGTH: 8 bases

TCTTTTAT 8

SEQ ID NO: 6

SEQUENCE TYPE : Amino acid

SEQUENCE LENGTH: 221 amino acids

MOLECULE TYPE: Sequence which includes variable regions of  
P1.15 protein

Leu	Gln	Leu	Thr	Glu	Pro	Pro	Ser	Lys	Ser	Gln	Pro	Gln	Val	Lys
1				5					10					15
Val	Thr	Lys	Ala	Lys	Ser	Arg	Ile	Arg	Thr	Gln	Ile	Ser	Asp	Phe
				20					25					30
Gly	Ser	Phe	Ile	Gly	Phe	Lys	Gly	Ser	Glu	Asp	Leu	Gly	Glu	Gly
				35					40					45
Leu	Lys	Ala	Val	Trp	Gln	Leu	Glu	Gln	Asp	Val	Ser	Val	Ala	Gly
				50					55					60

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	Gly	Gly	Ala	Thr	Gln	Trp	Gly	Asn	Arg	Glu	Ser	Phe	Val	Gly	Leu
					65					70					75
5	Ala	Gly	Glu	Phe	Gly	Thr	Leu	Arg	Ala	Gly	Arg	Val	Ala	Asn	Gln
					80					85					90
10	Phe	Asp	Asp	Ala	Ser	Gln	Ala	Ile	Asp	Pro	Trp	Asp	Ser	Asn	Asn
					95					100					105
	Asp	Val	Ala	Ala	Ser	Gln	Leu	Gly	Ile	Phe	Lys	Arg	His	Asp	Asp
					110					115					120
15	Met	Pro	Val	Ser	Val	Arg	Tyr	Asp	Ser	Pro	Asp	Phe	Ser	Gly	Phe
					125					130					135
	Ser	Gly	Ser	Val	Gln	Phe	Val	Pro	Ile	Gln	Asn	Ser	Lys	Ser	Ala
					140					145					150
20	Tyr	Thr	Pro	Ala	Tyr	His	Tyr	Thr	Arg	Gln	Asn	Asn	Ala	Asp	Val
					155					160					165
	Phe	Val	Pro	Ala	Val	Val	Gly	Lys	Pro	Gly	Ser	Asp	Val	Tyr	Val
25					170					175					180
	Ala	Gly	Leu	Asn	Tyr	Lys	Asn	Gly	Gly	Phe	Ala	Gly	Ser	Tyr	Ala
					185					190					195
30	Phe	Lys	Tyr	Ala	Arg	His	Ala	Asn	Val	Gly	Arg	Asn	Ala	Phe	Glu
					200					205					210
	Leu	Phe	Leu	Leu	Gly	Ser	Thr	Ser	Asp	Glu	Ala				
					215					220					

35

SEQ ID NO: 7

SEQUENCE TYPE : Amino acid

40

SEQUENCE LENGTH: 6 amino acids

MOLECULE TYPE: Sequence corresponding to the fusion site  
between N-terminal of P64k and P1.15

45

Gly	Asp	Ala	Leu	Gln	Leu
1				5	

50

55

SEQ ID NO: 8

SEQUENCE TYPE : Nucleotide

SEQUENCE LENGTH: 19 bases

MOLECULE TYPE: Sequence corresponding to the fusion of  
N-terminal from gene M-6 and from gene P1.15

GGCGACGCGC TGCAGTTGA

19

SEQ ID NO: 9

SEQUENCE TYPE : Amino acid

SEQUENCE LENGTH: 6 amino acids

MOLECULE TYPE: Sequence corresponding to the fusion site  
between C-terminal of P64k and P1.15

Glu Ala Asn Ala Tyr Glu  
1 5

SEQ ID NO: 10

SEQUENCE TYPE : Nucleotide

SEQUENCE LENGTH: 18 bases

MOLECULE TYPE: Sequence corresponding to the fusion of  
C-terminal from gene M-6 and from gene P1.15

GAAGCCAACG CGTACGAA

18

SEQ ID NO: 11

SEQUENCE TYPE : Amino acid

SEQUENCE LENGTH: 111 amino acids

MOLECULE TYPE: p64k N-terminal comprising homology region  
with "lypoil binding site" from E. coli Acetyl transferase

Met Ala Leu Val Glu Leu Lys Val Pro Asp Ile Gly Gly His Glu  
1 5 10 15

Asn Val Asp Ile Ile Ala Val Glu Val Asn Val Gly Asp Thr Ile  
20 25 30

Ala Val Asp Asp Thr Leu Ile Thr Leu Glu Thr Asp Lys Ala Thr  
35 40 45

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Met Asp Val Pro Ala Glu Val Ala Gly Val Val Lys Glu Val Lys
                    50                    55                    60
5 Val Lys Val Gly Asp Lys Ile Ser Glu Gly Gly Leu Ile Val Val
                    65                    70                    75
Val Glu Ala Glu Gly Thr Ala Ala Ala Pro Lys Ala Glu Ser Ala
                    80                    85                    90
10 Ala Ala Pro Arg Lys Lys Pro Leu Lys Cys Arg Trp Val Pro Gln
                    95                    100                    105
Ala Ala Gln Phe Gly Gly
15                    110

```

SEQ ID NO: 12

SEQUENCE TYPE : Amino acid

SEQUENCE LENGTH: 112 amino acids

MOLECULE TYPE: "lypoil binding site" from E. coli Acetyl-  
transferase

```

25 Val Lys Glu Val Asn Val Pro Asp Ile Gly Gly Asp Glu Val Glu
    1                    5                    10                    15
30 Val Thr Glu Val Met Val Lys Val Gly Asp Lys Val Ala Ala Glu
    20                    25                    30
Gln Ser Leu Ile Thr Val Glu Gly Asp Lys Ala Ser Met Glu Val
    35                    40                    45
35 Pro Ala Pro Phe Ala Gly Val Val Lys Glu Leu Lys Val Asn Val
    50                    55                    60
Gly Asp Lys Val Lys Thr Gly Ser Leu Ile Met Ile Phe Glu Val
40                    65                    70                    75
Glu Gly Ala Ala Pro Ala Ala Ala Pro Ala Lys Gln Glu Ala Ala
    80                    85                    90
45 Ala Pro Ala Pro Ala Ala Lys Ala Glu Ala Pro Ala Ala Ala Pro
    95                    100                    105
Ala Ala Lys Ala Glu Gly Lys
    110
50
55

```

SEQ ID NO: 13

SEQUENCE TYPE : Amino acid

SEQUENCE LENGTH: 481 amino acids

MOLECULE TYPE: P64k fragment comprising the homology region  
with Lipoamide Dehydrogenase from E. coli

5	Ser	Ala	Asp	Ala	Glu	Tyr	Asp	Val	Val	Val	Leu	Gly	Gly	Gly	Pro	1	5	10	15
15	Gly	Gly	Tyr	Ser	Ala	Ala	Phe	Ala	Ala	Ala	Asp	Glu	Gly	Leu	Lys	20	25	30	
20	Val	Ala	Ile	Val	Glu	Arg	Tyr	Lys	Thr	Leu	Gly	Gly	Val	Cys	Leu	35	40	45	
	Asn	Val	Gly	Cys	Ile	Pro	Ser	Lys	Ala	Leu	Leu	His	Asn	Ala	Ala	50	55	60	
25	Val	Ile	Asp	Glu	Val	Arg	His	Leu	Ala	Ala	Asn	Gly	Ile	Lys	Tyr	65	70	75	
	Pro	Glu	Pro	Ala	Leu	Asp	Ile	Asp	Met	Leu	Arg	Ala	Tyr	Lys	Asp	80	85	90	
30	Gly	Val	Val	Ser	Arg	Leu	Thr	Gly	Phe	Gly	Arg	Tyr	Gly	Glu	Lys	95	100	105	
	Arg	Lys	Val	Asp	Val	Ile	Gln	Gly	Asp	Gly	Gln	Phe	Leu	Asp	Pro	110	115	120	
35	His	His	Leu	Glu	Val	Ser	Leu	Thr	Ala	Gly	Asp	Ala	Tyr	Glu	Gln	125	130	135	
40	Ala	Ala	Pro	Thr	Gly	Glu	Lys	Lys	Ile	Val	Ala	Phe	Lys	Asn	Cys	140	145	150	
	Ile	Ile	Ala	Ala	Gly	Ser	Arg	Val	Thr	Lys	Leu	Pro	Phe	Ile	Pro	155	160	165	
45	Glu	Asp	Pro	Arg	Ile	Ile	Asp	Ser	Ser	Gly	Ala	Leu	Ala	Leu	Lys	170	175	180	
	Glu	Val	Pro	Gly	Lys	Leu	Leu	Ile	Ile	Gly	Gly	Gly	Ile	Ile	Gly	185	190	195	
50	Leu	Glu	Met	Gly	Thr	Val	Tyr	Ser	Thr	Leu	Gly	Ser	Arg	Leu	Asp	200	205	210	
55	Val	Val	Glu	Met	Met	Asp	Gly	Leu	Met	Gln	Gly	Ala	Asp	Arg	Asp	215	220	225	



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5	Leu	Val	Lys	Val	Trp	Gln	Lys	Gln	Asn	Glu	Tyr	Arg	Phe	Asp	Asn	230	235	240
	Ile	Met	Val	Asn	Thr	Lys	Thr	Val	Ala	Val	Glu	Pro	Lys	Glu	Asp	245	250	255
10	Gly	Val	Tyr	Val	Thr	Phe	Glu	Gly	Ala	Asn	Pro	Pro	Lys	Glu	Pro	260	265	270
	Gln	Arg	Tyr	Asp	Ala	Val	Leu	Val	Ala	Ala	Gly	Arg	Ala	Pro	Asn	275	280	285
15	Gly	Lys	Leu	Ile	Ser	Ala	Glu	Lys	Ala	Gly	Val	Ala	Val	Thr	Asp	290	295	300
	Arg	Gly	Phe	Ile	Glu	Val	Asp	Lys	Gln	Met	Arg	Thr	Asn	Val	Pro	305	310	315
20	His	Ile	Tyr	Ala	Ile	Gly	Asp	Ile	Val	Gly	Gln	Pro	Met	Leu	Ala	320	325	330
	His	Lys	Ala	Val	His	Glu	Gly	His	Val	Ala	Ala	Glu	Asn	Cys	Ala	335	340	345
	Gly	Thr	Lys	Ala	Tyr	Phe	Asp	Ala	Ala	Val	Ile	Pro	Gly	Val	Ala	350	355	360
30	Tyr	Thr	Ser	Pro	Glu	Val	Ala	Trp	Val	Gly	Glu	Thr	Glu	Leu	Ser	365	370	375
	Ala	Lys	Arg	Pro	Ala	Gly	Lys	Ile	Thr	Lys	Ala	Asn	Phe	Pro	Trp	380	385	390
35	Ala	Ala	Ser	Gly	Arg	Ala	Ile	Ala	Asn	Gly	Cys	Asp	Lys	Pro	Phe	395	400	405
	Thr	Lys	Leu	Ile	Phe	Asp	Ala	Glu	Thr	Gly	Arg	Ile	Ile	Gly	Gly	410	415	420
	Gly	Ile	Val	Gly	Pro	Asn	Gly	Gly	Asp	Met	Ile	Ala	Lys	Ser	Ala	425	430	435
45	Leu	Pro	Ser	Lys	Leu	Gly	Cys	Asp	Ala	Ala	Asp	Val	Gly	Lys	Thr	440	445	450
	Ile	His	Pro	Arg	Pro	Thr	Leu	Gly	Glu	Ser	Ile	Gly	Met	Ala	Ala	455	460	465
50	Glu	Val	Ala	Leu	Gly	Thr	Cys	Thr	Asp	Leu	Pro	Pro	Gln	Lys	Lys	470	475	480
55	Lys																	

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SEQ ID NO: 14

SEQUENCE TYPE : Amino acid

SEQUENCE LENGTH: 472 bases

MOLECULE TYPE: Segment of E. coli Lipoamide Dehydrogenase  
with homology to P64k protein

5	Ser	Thr	Glu	Ile	Lys	Thr	Gln	Val	Val	Val	Leu	Gly	Ala	Gly	Pro	1	5	10	15
15	Ala	Gly	Tyr	Ser	Ala	Ala	Phe	Arg	Cys	Ala	Asp	Leu	Gly	Leu	Glu	20	25	30	
20	Thr	Val	Ile	Val	Glu	Arg	Tyr	Asn	Thr	Leu	Gly	Gly	Val	Cys	Leu	35	40	45	
	Asn	Val	Gly	Cys	Ile	Pro	Ser	Lys	Ala	Leu	Leu	His	Val	Ala	Lys	50	55	60	
25	Val	Ile	Glu	Glu	Ala	Lys	Ala	Leu	Ala	Glu	His	Gly	Ile	Val	Phe	65	70	75	
	Gly	Glu	Pro	Lys	Thr	Asp	Ile	Asp	Lys	Ile	Thr	Trp	Lys	Glu	Lys	80	85	90	
30	Val	Ile	Asn	Gln	Leu	Thr	Gly	Gly	Leu	Ala	Gly	Met	Ala	Lys	Gly	95	100	105	
	Arg	Lys	Val	Lys	Val	Val	Asn	Gly	Leu	Gly	Lys	Phe	Thr	Gly	Ala	110	115	120	
35	Asn	Thr	Leu	Glu	Val	Glu	Gly	Glu	Asn	Gly	Lys	Thr	Val	Ile	Asn	125	130	135	
40	Phe	Asp	Asn	Ala	Ile	Ile	Ala	Ala	Gly	Ser	Arg	Pro	Ile	Gln	Leu	140	145	150	
	Pro	Phe	Ile	Pro	His	Glu	Asp	Pro	Arg	Ile	Trp	Asp	Ser	Thr	Asp	155	160	165	
45	Ala	Leu	Glu	Leu	Lys	Glu	Val	Pro	Glu	Arg	Leu	Leu	Val	Met	Gly	170	175	180	
	Gly	Gly	Ile	Ile	Gly	Leu	Glu	Met	Gly	Thr	Val	Tyr	His	Ala	Leu	185	190	195	
50	Gly	Ser	Gln	Ile	Asp	Val	Val	Glu	Met	Phe	Asp	Gln	Val	Ile	Pro	200	205	210	
55	Ala	Ala	Asp	Lys	Asp	Ile	Val	Lys	Val	Phe	Thr	Lys	Arg	Ile	Ser	215	220	225	

5	Lys	Lys	Phe	Asn	Leu	Met	Leu	Glu	Thr	Lys	Val	Thr	Ala	Val	Glu	230	235	240
	Ala	Lys	Glu	Asp	Gly	Ile	Tyr	Val	Thr	Met	Glu	Gly	Lys	Lys	Ala	245	250	255
10	Pro	Ala	Glu	Pro	Gln	Arg	Tyr	Asp	Ala	Val	Leu	Val	Ala	Ile	Gly	260	265	270
	Arg	Val	Pro	Asn	Gly	Lys	Asn	Leu	Asp	Ala	Gly	Lys	Ala	Gly	Val	275	280	285
15	Glu	Val	Asp	Asp	Arg	Gly	Phe	Ile	Arg	Val	Asp	Lys	Gln	Leu	Arg	290	295	300
	Thr	Asn	Val	Pro	His	Ile	Phe	Ala	Ile	Gly	Asp	Ile	Val	Gly	Gln	305	310	315
20	Pro	Met	Leu	Ala	His	Lys	Gly	Val	His	Glu	Gly	His	Val	Ala	Ala	320	325	330
	Glu	Val	Ile	Ala	Gly	Lys	Lys	His	Tyr	Phe	Asp	Pro	Lys	Val	Ile	335	340	345
25	Pro	Ser	Ile	Ala	Tyr	Thr	Glu	Pro	Glu	Val	Ala	Trp	Val	Gly	Leu	350	355	360
	Thr	Glu	Lys	Glu	Ala	Lys	Glu	Lys	Gly	Ile	Ser	Tyr	Glu	Thr	Ala	365	370	375
30	Thr	Phe	Pro	Trp	Ala	Ala	Ser	Gly	Arg	Ala	Ile	Ala	Ser	Asp	Cys	380	385	390
	Ala	Asp	Gly	Met	Thr	Lys	Leu	Ile	Phe	Asp	Lys	Glu	Ser	His	Arg	395	400	405
35	Val	Ile	Gly	Gly	Ala	Ile	Val	Gly	Thr	Asn	Gly	Gly	Glu	Leu	Leu	410	415	420
	Gly	Glu	Ile	Gly	Leu	Ala	Ile	Glu	Met	Gly	Cys	Asp	Ala	Glu	Asp	425	430	435
40	Ile	Ala	Leu	Thr	Ile	His	Ala	His	Pro	Thr	Leu	His	Glu	Ser	Val	440	445	450
	Gly	Leu	Ala	Ala	Glu	Val	Phe	Glu	Gly	Ser	Ile	Thr	Asp	Leu	Pro	455	460	465
45	Asn	Pro	Lys	Ala	Lys	Lys	Lys									470		

55  
**Claims**

1. A recombinant polynucleotide, comprising a nucleotide sequence coding for a protein P64k of Neisseria

meningitidis, said protein P64k essentially having the amino acid sequence shown in SEQ ID NO:1.

2. A recombinant polynucleotide according to claim 1, wherein said nucleotide sequence coding for the protein P64k of *N. meningitidis* essentially consists of the nucleotide sequence shown in SEQ ID NO:1.
3. A recombinant polynucleotide according to claim 1 or 2, further comprising a nucleotide sequence of a cloning or expression vector.
4. A transformed microorganism, containing a recombinant polynucleotide according to any of claims 1 to 3.
5. A transformed microorganism according to claim 4, which is capable of expressing the protein P64k of *N. meningitidis*.
6. A transformed microorganism according to claim 5, which is an *Escherichia coli* strain, e.g. *E. coli* strain HB101, transformed with an expression vector containing a nucleotide sequence coding for the protein P64k of *N. meningitidis*, e.g. the expression vector pM-6.
7. A recombinant proteinaceous substance, comprising an amino acid sequence corresponding to the amino acid sequence of at least a part of a protein P64k of *N. meningitidis*, said protein P64k essentially having the amino acid sequence shown in SEQ ID NO:1.
8. A recombinant proteinaceous substance according to claim 7, which is a fusion protein or a protein/polysaccharide conjugate comprising the amino acid sequence of protein P64k of *N. meningitidis*.
9. A vaccine composition, comprising a recombinant protein according to claim 7 or 8, together with a suitable carrier, diluent or adjuvant.
10. A vaccine composition, comprising a lipoamide dehydrogenase or acetyl transferase capable of inducing antibodies which can bind a protein P64k of *N. meningitidis*, together with a suitable carrier, diluent or adjuvant.
11. Monoclonal antibody, raised against a recombinant proteinaceous substance according to claim 7 or 8, or against a lipoamide dehydrogenase or acetyl transferase, and capable of binding a protein P64k of *N. meningitidis*.
12. A process for preparing a protein P64k of *Neisseria meningitidis*, or a fusion protein comprising protein P64k, said protein P64k essentially having the amino acid sequence shown in SEQ ID NO:1, comprising the steps of transforming a microorganism with an expression vector containing a nucleotide sequence coding for said protein P64k, or said fusion protein, culturing the transformed microorganism to obtain expression of said protein P64k, or said fusion protein, and isolating said expression product.
13. A method for the isolation and expression of a gene which codes for a protein belonging to the outer membrane of *N. meningitidis* and its use in vaccine preparations, wherein the gene from the strain of *N. meningitidis* B:4:P1.15, identified as M-6, is obtained from the screening of a genomic library in the EMBL 3, and is cloned and expressed in a suitable host, coding for a protein of 64kDa belonging to the outer membrane of *N. meningitidis* which has bactericidal activity against different serogroups, serotypes and subtypes of *N. meningitidis*.
14. A nucleotide sequence obtained by the method of claim 13, characterized in that the sequence is corresponding with the M-6 gene and codes for the P64k protein, identified in the sequence listing with number 1.
15. A recombinant DNA according to claims 13 and 14, characterized in that it is a molecule which contains the M-6 gene which codes for P64k protein.

16. A recombinant DNA according to claim 15, characterized in that it is a phage, a plasmid or an expression vector.
17. A recombinant DNA according to claims 15 and 16, characterized in that it is the phage EMBL 3, plasmid pM-1 and expression vector pM-6.
18. A transformed microorganism according to the preceding claims, characterized in that it results from the transformation of a suitable host, carries the M-6 gene, expresses high levels of P64k protein and maintains good viability and cellular stability.
19. A transformed microorganism according to claim 18, characterized in that it is the clone HBM64 which is obtained from the transformation of E. coli host strain HB101 with the expression vector pM-6, and it presents high stability and viability and expression levels of P64k protein higher than 25 % of the total protein of the cell.
20. A recombinant protein obtained according to the preceding claims, characterized in that it essentially has the amino acid sequence shown in the sequence listing under SEQ ID NO:1.
21. Protein P64k according to preceding claims characterized in that it is the direct result of the expression of the M-6 gene as well as any peptide which has important immunological regions obtained by chemical synthesis or enzymatic degradation of P64k protein and its use in fusion proteins and polysaccharide protein conjugates for monovalent and multivalent vaccine preparations.
22. A vaccine preparation comprising protein P64k and at least one carrier, diluent or adjuvant used for vaccine preparations, as well as comprising any protein of Lipoamide dehydrogenase or Acetyl transferase from other organism or modification thereof, which is able to induce antibodies against the P64k protein.

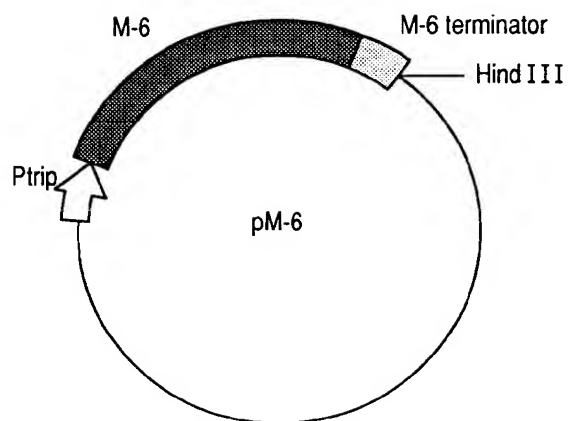


FIG. 1

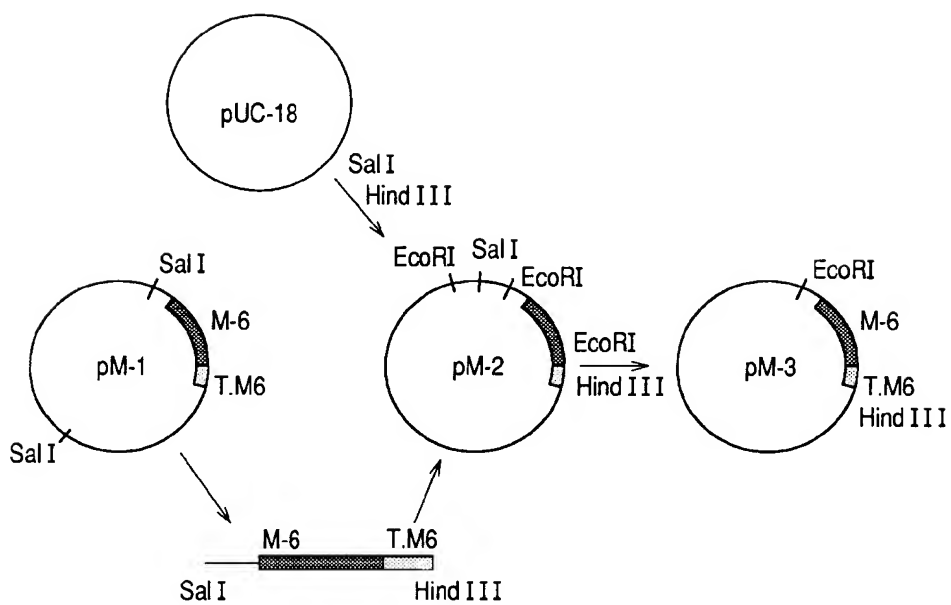
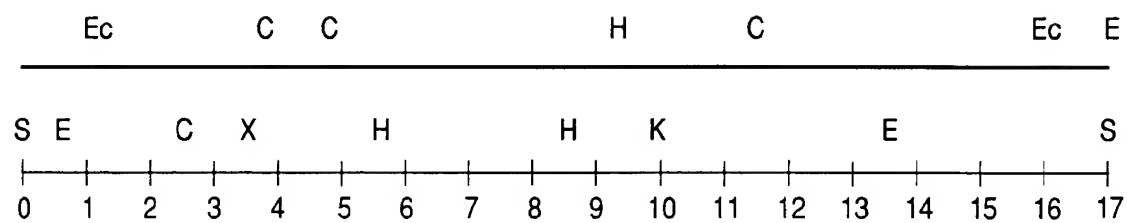


FIG. 2



S. Sal I; E. EcoRV; Ec. EcoRI; C. Cla I;  
X. Xho I; H. Hind III; K. Kpn I.

FIG. 3

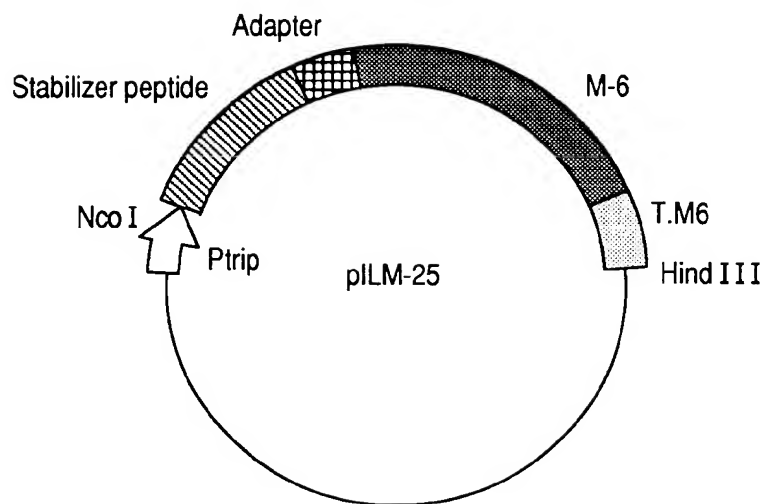


FIG. 4

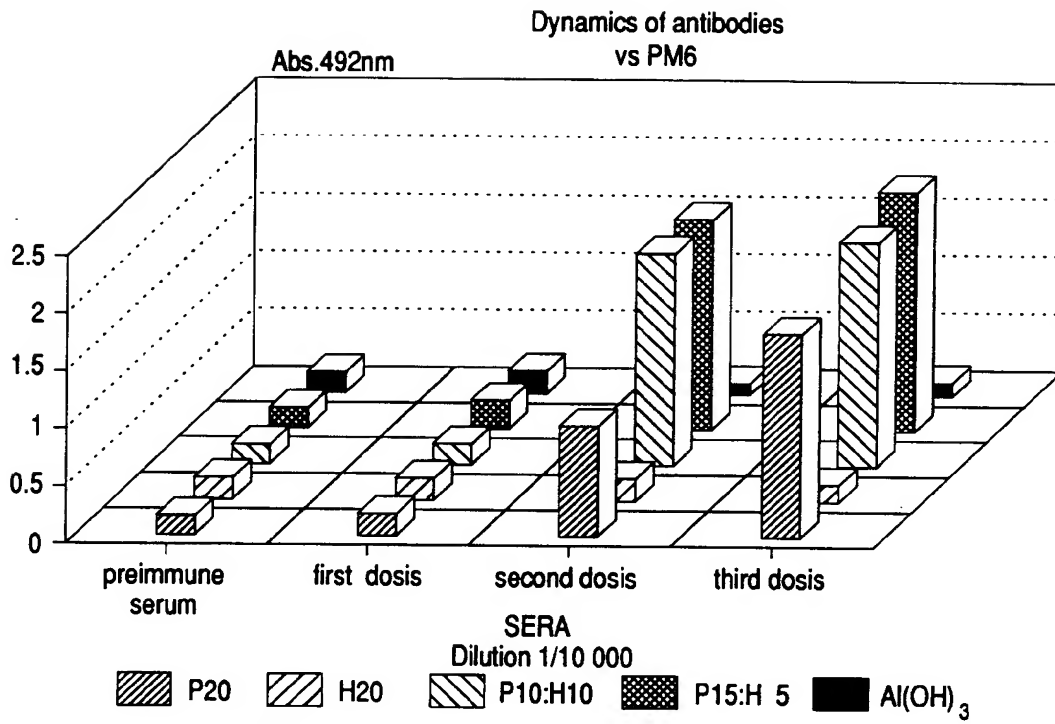


FIG. 5

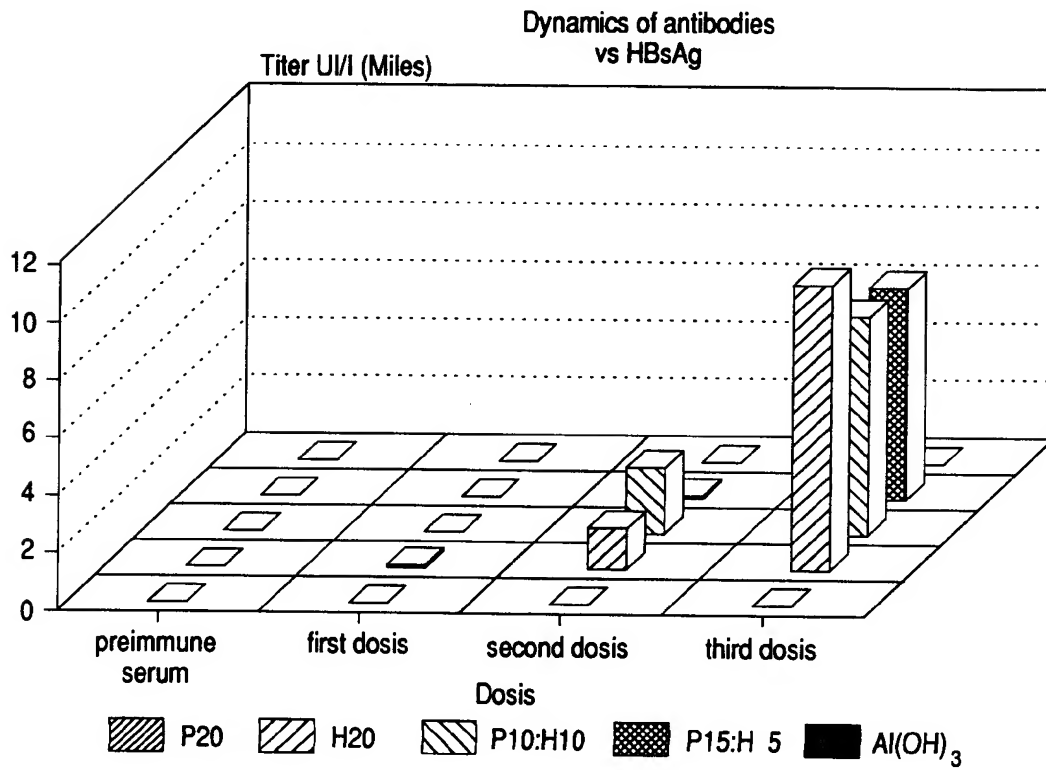


FIG. 6